

FIGURE 1A

1	GNTCTAGAA	TAGTGGATCC	CCCCGGGCTG	CAGGAATTCC	GACGGCCCTT	GGAAGGGCTC	TGGTGGGGCT	GAGCGCTCTG	CCGCGGGGGC	GCGGCACAG
	CNAGATCTTN	ATCACCTAGG	GGGGCCCGAC	GTCTTAAGG	CTGCCGGGA	CCTTCCCGAG	ACCACCCCGA	CTCGCGAGAC	GGCGCCCGCG	CGCCCGTGTC
101	CAGGAAGCAG	GTCCCGCTGG	CGCGTGGGG	CATCAGCTAC	CGGGTGGTTC	CGGGCTGAAG	AGCCAGGCAG	CAAAGGCAGC	CACCCCGGGG	GGTGGGGCAG
	GTCTTCTGTC	CAGCGGCACC	CGCGACCCCG	GTAGTCGATG	GCCCCACCCAG	GCCCGACTTC	TCGGTCCGTC	GGTTCGCTCG	GTGGGGCCCC	CCACCCGCTG
201	TTTTGGGGAG	TTGGTGCCCG	GCCCCCAGG	CCTTGGCGGG	GTCTATGGGG	CCCCCATTC	TGGGCCGGGG	GGCGTGCGAG	TCGGGGCCCTT	GCTGTGCTG
	AAACCCCTC	AACCACGGG	CGGGGGTCC	GGAACCGCCC	CAGTACCCCG	GGGGGGTAAG	ACCCGGCCCC	CCGCACGCTC	AGCCCCGGGA	CGACGACGAC
1					MetGlyP	roProHisSe	rGlyProGly	GlyValArgV	alGlyAlaLe	uLeuLeuLeu
301	GGGGTTTTGG	GGCTGGTGTG	TGGGCTCAGC	CTGGAGCCCTG	TCTACTGGAA	CTCGGCGAAT	AAGAGGTTC	AGGCAGAGGG	TGGTTATGTG	CTGTACCCCTC
	CCCCAAAACC	CCGACCACAG	ACCCGAGTCG	GACCTCGGAC	AGATGACCTT	GAGCCGCTTA	TTCTCCAAAG	TCCGTCTCCC	ACCAATACAC	GACATGGGAG
401	GlyValLeuG	lyLeuValSe	rGlyLeuSer	LeuGluProV	alTyTrpAs	nSerAlaAsn	LysArgPheG	InAlaGluG	yGlyTyrrVal	LeuTyrrProGln
54	IleGlyAs	pArgLeuAsp	LeuLeuCysP	roArgAlaAr	gProProGly	ProHisSerS	erProAsnTy	rGluPheTyrr	LysLeuTyrrL	euValGlyGly
501	TGCTCAGGGC	CGGCGCTGTG	AGGCACCCCG	TGCCCCAAAC	CTCTTCTTCA	CTTGTGATCG	CCAGACCTTG	GATCTCCGCT	TCACCATCAA	GTTCACAGGAG
	ACGAGTCCCG	GCCGCGACAC	TCCGTGGGG	ACGGGGTTTG	GAGGAAGAGT	GAACACTAGC	GGGTCTGGAC	CTAGAGCGCA	AGTGTAGTTC	CAAGGTCCCTC
87	AlaGlnGly	ArgArgCysG	luAlaProPr	oAlaProAsn	LeuLeuLeuT	hrCysAspAr	gProAspLeu	AspLeuArgP	heThrIleLy	sPheGlnGlu
601	TATAGCCCTA	ATCTCTGGGG	CCACGAGTTC	CGCTCGCAC	ACGATTACTA	CATCATTTGCC	ACATCGGATG	GGACCCGGGA	GGGCTGGAG	AGCCTGCAGG
	ATATCGGGAT	TAGAGACCCC	GGTCTCAAG	GCGAGCGTGG	TGCTAATGAT	GTAGTAACGG	TGTAGCCTAC	CCTGGGCCCT	CCCGACCTC	TCGGACGTCC
120	TyrSerProA	snLeuTrpGl	yHisGluPhe	ArgSerHisH	isAspTyrrTy	rIleIleAla	ThrSerAspG	lyThrArgG	uGlyLeuGlu	SerLeuGlnGly
701	GAGGTGTGTG	CCTAACACAG	GGCATGAAGG	TGCTTCTCCG	AGTGGGACAA	AGTCCCGCAG	GAGGGGCTGT	CCCCCGAAAA	CCTGTGTCTG	AAATGCCCAT
	CTCCACACAC	GGATTGTCT	CCGTACTTCC	ACGAAGAGSC	TCACCCTGTT	TCAGGGGCTC	CTCCCCGACA	GGGGGCTTTT	GGACACAGAC	TTTACGGGTA
154	GlyValCy	sLeuThrArg	GlyMetLysV	alLeuLeuAr	gValGlyGln	SerProArgG	lyGlyAlaVa	lProArgLys	ProValSerG	luMetProMet
187	GGAAAGAGAC	CGAGGGGCAG	CCCACAGCCT	GGAGCCTGGG	AAGGAGAACC	TGCCAGGTGA	CCCCACCCAG	AATGCAACCT	CCCGGGGTGC	TGAAGGCCCC
	CCTTTCTCTG	GCTCCCCGTC	GGGTGTGCGA	CCTCGGACCC	TTCTCTTTGG	ACGGTCCACT	GGGGTGGTCG	TTACGTTTGA	GGGCCCCACG	ACTTCCGGGG
187	GluArgAsp	ArgGlyAlaA	laHisSerLe	uGluProGly	LysGluAsnL	euProGlyAs	pProThrSer	AsnAlaThrS	erArgGlyAl	aGluGlyPro
901	CTGCCCCCTC	CCAGCATGCC	TGCAGTGGCT	GGGCGACGAG	GGGGGCTGGC	GCTGCTCTTG	CTGGGCGTGG	CAGGGGCTGG	GGGTGCCATG	TGTTGGCGGA
	GACGGGGGAG	GSTCGTACCG	ACGTACCCGA	CCCCCGTCTC	CCCCCGACCG	CGACGAGAAC	GACCCGACCC	GTCCCGGACC	CCCACGGTAC	ACAAACCCCT
220	LeuProProp	roSerMetPr	oAlaValAla	GlyAlaAlaG	lyGlyLeuAl	aLeuLeuLeu	LeuGlyValA	laGlyAlaGl	yGlyAlaMet	CysTrpArgArg
1001	GACGGCGGGC	CAAGCCTTCG	GAGAGTCGCC	ACCCCTGGTCC	TGGCTCTTTC	GGGAGGGGAG	GGTCTCTGGG	CCTGGGGGGT	GGAGGTGGGA	TGGGACCTCG
	CTGCCGCCCG	GTTTCGGAAGC	CTCTCAGCGG	TGGGACCAGG	ACCGAGGAAG	CCCTCCCTTC	CCAGAGACCC	GGACCCCTCA	CCTCCACCCCT	ACCTGGGAGC
254	ArgArgAl	alysProSer	GluSerArgH	isProGlyPr	oglySerPhe	GlyArgGlyG	lySerLeuG	yLeuGlyGly	GlyGlyGlyM	etGlyProArg
1101	GGAGGCTGAG	CCTGGGGGAG	TAGGATAGC	TCTCGGGGGT	GGCGGGGCTG	CAGATCCCCC	CTTCTGCCCC	CAGTATGAGA	AGGTAGTGG	TGACTATGGG
	CCTCCGACTC	GGACCCCTCG	ATCCCTATCG	AGACGCCCCA	CCGCCCCGAC	GTCATAGGGG	GAAGACGGGG	GTGACTACTCT	TCCACTCACC	ACTGATACCC
287	GluAlaGlu	ProGlyGluL	euGlyIleAl	aleuArgGly	GlyGlyAlaA	laAspProPr	opheCysPro	HistTyrrGluL	ysValSerG	yAspTyrrGly

FIGURE 1B

1201 CATCTGTGT ATATCGTGCA GGATGGGCCC CCCAGAGCC CTCCAAACAT CTACTACACA TCGATTTCCTG TGTGGAGTG GCCATATTG CATACGATAC
GTAGGACACA TATAGCACGT CCTACCCGGG GGGTCTCGG GAGTTTGTGAT GATGATGTGT AGCTAAAGAC ACAACCTCAC CGGTATAAC GPATGCTATG
320 HisProValT yrIleValG1 nAspGlyPro ProGlnSerP roProAsnI1 eYrTyrThr SerIleSerV alLeuGluTr pProIleLeu HisThrIleGln
1301 AACTGTTTTT CATGCGATCC AAGTGCTCCC GTGTCACATAC ATTCTTATTT CCTGTGCAAG TTATTACGAC ATCGACTTGC CGGATGACTT CATTTAGCTT
TTGACAAAA GTACGCTAGG TTCACGAGGG CACAGTGATG TAAGAATAAA GGACACGTTT AATAATGCTG TAGCTGAACG GCCTACTGAA GTAATTCGAA
354 LeuPhePh eMetArgSer LysCysSerA rgValThrTh rPheLeuPhe ProValGlnV alIleThrTh rSerThrCys ArgMetThrS erPheSerPhe
1401 TACCACCCCTG AACCCATCCA TGCAGGCCCTG CAGAGCACAG ATGGGGGAAT TCCGAATCAG ATGGTGTTC TGGGGGACACA GGATCCTGGG TACGGCTCTG
ATGGTGGGAC TTGGGTAGGT ACGTCCGGAC GTCTCGTGTG TACCCCTTA AGGCTTAGTC TACCACAAAAG ACCCCCTGT CCTAGGACCC ATGCCGAGAC
387 ThrThrLeu AsnProSerM etGlnAlaCy sArgAlaGln MetGlyGluP heArgIleAr gTrpCysPhe TrpGlyAspA rgIleLeuG1 yThrAlaLeu
401 TTTGTGCTTG TGCTTATCT TCTTCTTGGG AGGCTGAATA TGCATCAGAC GACACTGCTC CGGCAACGGG CCAGTGTGGA GGCGGAAGCC GGCCAGCATG
AAACACGAAC ACGAATAAGA AGAAGAACCC TCCGACTTAT ACGTAGTCTG CTGTGACGAG GCCGTTGCC GGTACACACT CCGCTTCGG CCGTTCGTAC
420 PheValLeuV alLeuIleLe uLeuLeuGly ArgLeuAsnM etHisGlnTh rThrLeuLeu ArgGlnArgA laSerValG1 uAlaGluAla GlyGlnHisGly
1601 GTCCCCCTGT ATAGGATTGA AAGAGCTACT GAGAATAGGG GGCTTCTCAA TGAGAGAGCG GAGGCTGCTG TTATCATGGG AACCAAGCAG ATCAATCATC
CAGGGGACAC TATCCTAACT TTCTCGATGA CTCTTATCCC CCGAAGAGTT ACTCTCTGCG CTCCGACGAC AATAGTACCC TTGGTCCGTC TAGTTAGTAG
454 ProLeu
1701 CCTGGCAGGT CAGGCAGGAA GTTACTTTAGC TTCTCCTTCA CCTTCTTCCC ACAGAAATTA TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTCTG
GGACCGTCCA GTCCGTCCTT CAATGAATCG AAGAGGAAGT GGAAGAAGGG TGCTCTAAAT AATATCCGAA CAAGGTTCAA CATCACACAC TAGTCTAAGC
1801 TGCTGCCCTGT CAGCTCTGTG CTACCTGGCA GTTCCCTTCA TGGAAATTCGA TATCAAGCTT ATCGATACCG TCGACCT
ACGACGGACA GTCGAGACAC GATGGACCGT CAAGGGGAGT ACCTTAAGCT ATAGTTCGAA TAGCTATGGC AGCTGGA

FIGURE 2A

1 GNTCTAGAA TACTGCATCC CCCCAGGCTG CAGGAATTCC GACCCGCCCTT CCAAGGGCTC TGGTGGGGCT GAGGGCTCTG CCCCCTGGCC GCGGGGACAC
 CNAATCTTN ATCAGCTAGG GCGGCCCCAC GTCTTTTAGC CTGCGGGGA CATTCTCGAG ACCACCCCGA CCGGCCCCCG GCGGCTGGTG
 101 CAGGAGACAC CTCCCGCTGG GCGCTGGGG CATTAGCTAC CCGGCTGCTC CCGCTGAAG ACCCAGGCTC CCAAGGACAC CACCCGCTGG GCTGGGGGAC
 GTCTTCTCTC CAGGCGCAC CCGGACCTCC GTAGCTGATG CCCCACACAG CCCCACCTTC TCGTCCGCTC GGTTCGCTGG GTGGGGCTCC CCAACCGCTG
 201 TTGGGGGGAG TTGGTGCCTC GCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC
 AAACCCCTTC AACCAAGGG GCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC
 1 MetGlyP roProHisP GlyValArgV alGlyAlaLe uLeuLeuLeu
 301 CCGGTTTTCG GCTGCTGCTC TCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC
 CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC
 20 GlyValLeuG lylleuValse rGlyLeuSer LeuGluProV altyrPAs nSerAlaAsn LysArgPheG lnaAlaGluG lGlyTyrVal LeuTyrProGln
 401 AGATCGGGGA CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC
 TCTAGCCCCC TCTAGCCCCC TCTAGCCCCC TCTAGCCCCC TCTAGCCCCC TCTAGCCCCC TCTAGCCCCC TCTAGCCCCC TCTAGCCCCC TCTAGCCCCC
 54 lloglyAs pArgGluAsp leuLeuCySP roArgAlaAr gProProGly ProHisSer erProAsnTy rGluPheTyr LysLeuTyrL cuValGlyGly
 501 TGCTCAGGGC CCGGCTGCTC AGGACCCCCC TGCCCCAAC CTCTTCTCTC CTTGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC
 ACCAGCTCTG CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC
 8/ AlaGlnGly ArgArgCySG luAlaProPr oAlaProAsn LeuLeuLeuT hCysAspAr gProAspLeu AspLeuArgp heuTrileLy spheGlnGlu
 601 TATAGAGCTA ATCTCTGGG CACGAGCTC CCGTCTGCTC CCGTCTGCTC CCGTCTGCTC CCGTCTGCTC CCGTCTGCTC CCGTCTGCTC CCGTCTGCTC
 ATATCGGAT TAGAGACCCC GGTGCTCAAG CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC
 120 TyrSerProA snLeuTrpG lHisGluPhe ArgSerHis isAspTyrTy rIleIleAla ThrSerAspG lyThrArgG lGlyLeuGlu SerLeuGlnGly
 701 GAGGCTGCTC CCAACACCA CCGATGAAAC TGCTTCTCCG ACTGGGACAA AGTCCCTCCG CAGGGCTCTT CCCCAGAAA CCTGTGCTC AATGCCCCAT
 CTCCACACAC GGATTGCTC CCGTACTTCC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC
 154 GlyValCy sLeuThrArg GlyMetLysv alLeuLeuAr gValGlyGln SerProArgG lGlyAlaVa lProArgLys ProValSerG luMetProMet
 801 GGAAGAGAC CAGGGGGAC CCAACAGCT CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC CCGGCTGCTC
 CTTTCTCTG CTTTCTCTG CTTTCTCTG CTTTCTCTG CTTTCTCTG CTTTCTCTG CTTTCTCTG CTTTCTCTG CTTTCTCTG CTTTCTCTG
 187 GluArgAsp ArgGlyAlaAla lHisSerLeu uGluProGly LysGluAsnL euproHiser pProHiser AsnAlaThrS erArgGlyAla aGlnGlyPro
 901 CTTTCTCTG CCGGCTGCTC TCGGCTGCTC GCGGCTGCTC GCGGCTGCTC GCGGCTGCTC GCGGCTGCTC GCGGCTGCTC GCGGCTGCTC GCGGCTGCTC
 GAGGCTGCTC GAGGCTGCTC GAGGCTGCTC GAGGCTGCTC GAGGCTGCTC GAGGCTGCTC GAGGCTGCTC GAGGCTGCTC GAGGCTGCTC GAGGCTGCTC
 220 LeuProProp roSerMetPr oAlaValAla GlyAlaAlaC lGlyLeuAla leuLeuLeu LeuGlyVala laGlyAlaG lGlyAlaMet. CysTrpArgArg
 1001 GAGGCTGCTC CAGGCTGCTC GAGGCTGCTC GAGGCTGCTC GAGGCTGCTC GAGGCTGCTC GAGGCTGCTC GAGGCTGCTC GAGGCTGCTC GAGGCTGCTC
 CTTTCTCTG GTTTCTCTG CTTTCTCTG CTTTCTCTG CTTTCTCTG CTTTCTCTG CTTTCTCTG CTTTCTCTG CTTTCTCTG CTTTCTCTG
 254 ArgArgAla lLysProSer GluSerArgH lsProGlyPr oglySerPhe GlyArgGlyG lYserLeuCl yLeuGlyGly GlyGlyGlyG lYleuGlyGly etilYleuGlyGly

FIGURE 2B

1101 GGAGGCTGAG CCTGGGGAGC TAGGAATAGC TCTGGGGGT GCGGGGGGTG CAGATCCCCC CTCTGCCCC CACTATGAGA AGGTGAGTGG TGACTATGGG
 287 GluAlaGlu ProGlyGluL euGlyIleAl aLeuArgGly GlyGlyAlaA laaspProPr oPheCysPro oPheCysPro HisTyxGluL ysValserGL yAspTyxGly
 1201 CATGCTGTGT ATATCGTGA ATATCGTGA GGTGGGGCC CCCCAGAGCC CTCCAAACAT CTACTACAAG GPATGAGGGC TCCCTCAGC TGGCTATCTT CAATCCAGCC
 320 HisProValT yIleValGL nAspGlyPro ProGlnSerP roProAsnII eTyxTyxLys Valop* CATACTCCCG AGGAGAGTGC ACCGATAGGA CTTAGGTGCG
 1301 CTCTCTGGGG TGTCTCTCCA GTTAAATTC TGGTTTGGG GACACCTCTA ACATCTCGG CCCCTGTGCC CCCCAGAGCC CTTCACCTCT CCCGGGTGCT
 GAAGAACCCC ACGAGGAGGT CAATTAAGG ACCAACTCC CTGTGGAGAT TGTAGAGCCG GCGGACACGG GCGGTGCGG GAAGTAGGA GGGCCGAGCA
 1401 GTCTCTGGTCT CCACPTTTAG GATTCCTTAG GATTCCTTAG GATTCCTTAG GATTCCTTAG GATTCCTTAG GATTCCTTAG GATTCCTTAG GATTCCTTAG
 CAGGAGCAGA GGTGAATAATC CTAGGAATC CTAGGAATC CTAGGAATC CTAGGAATC CTAGGAATC CTAGGAATC CTAGGAATC CTAGGAATC CTAGGAATC
 1501 ATCTCTTTTC CTGGGGAGG GGCACAGGCT CAGCTCTCTC TCTGACCATG ACCAGGCTT CCTTGTGCC CCTTGTGCC CCTTGTGCC CCTTGTGCC
 TAGGAAAAAG GAACCCCTCC CCGTGTCCGA GTCCGAGGAG AGACTGGTAC TGGTCCGTA GGAACAGGG GGAACAGGG GGAACAGGG GGAACAGGG
 1601 GGCACACCTT TGGTGGCAC GCGCTCTCTT CTGGCTCTCA CTGGTCTCTT CTGGCTCTCT CTGGCTCTCT CTGGCTCTCT CTGGCTCTCT CTGGCTCTCT
 CCGGTGAAA ACCAACCGTG GCGGAAGAA GACGAGAGT GACCAAGA GACGAGAGT GACCAAGA GACGAGAGT GACCAAGA GACGAGAGT GACCAAGA
 1701 CTCTCTTAGC ATCTCTCTCC CCACATCTCC TTGACCTCTT TTGACCTCTT TTGACCTCTT TTGACCTCTT TTGACCTCTT TTGACCTCTT TTGACCTCTT
 GAAGGGAATG TAGGAGGAGG CCGTGTAGAG AAGTGGGAG AACCAAGAA TAGGACACGG AGAGGTAGA GAGGTAGA GAGGTAGA GAGGTAGA GAGGTAGA
 1801 CTTAGCTTTT AGCCCCCTT CTGACCTCTC ATACCTACCA CTGCTCTCAG TCTGCTCAG ATGCGGGCTT TATGCGGCTT TATGCGGCTT TATGCGGCTT
 GAATCGAAG TCGGGGGGA GACTGGAG GACTGGAG GACTGGAG GACTGGAG GACTGGAG GACTGGAG GACTGGAG GACTGGAG GACTGGAG
 1901 CTCAGGCCAT GGCAGGAGG GCTCCATCTT CTGGCTCTG CAGGCTCTT CAGGCTCTT CAGGCTCTT CAGGCTCTT CAGGCTCTT CAGGCTCTT
 GAGTCCGGTA CCGGTGCTC CAGGTAAGA CAGGTAAGA CAGGTAAGA CAGGTAAGA CAGGTAAGA CAGGTAAGA CAGGTAAGA CAGGTAAGA
 2001 AGAAGAGTGT TCCCGTTTGT TCCAGTGGCC ATATGCAAGA TATGAACCGG TGGGACATG TATGAGTGT TATGAGTGT TATGAGTGT TATGAGTGT
 TCTTCTTCA AGGCAAAAC AGGTCAACGG TATCGTCT TATCGTCT TATCGTCT TATCGTCT TATCGTCT TATCGTCT TATCGTCT TATCGTCT
 2101 GAAGTCACTT GCTCCAGAGA AGAGGTGACC AGGCTGGAC AGGCTGGAC AGGCTGGAC AGGCTGGAC AGGCTGGAC AGGCTGGAC AGGCTGGAC
 CTTCACCTGA CGAGGCTGT TCTCCACTGG TCCGGGCTGT TCCGGGCTGT TCCGGGCTGT TCCGGGCTGT TCCGGGCTGT TCCGGGCTGT TCCGGGCTGT
 2201 GACAGGAAGT AGCATCTGT NAACAGGAAG TGGTCTGGCT GGAACCTCAA GTGGCTTAGT CTGGGGGATC AGGAGGTGG AGGTGGATGG TCTTATTCT
 CTCTCTTCA TCGTGAAGAC TTTGTCTTTC ACCAGACCGA CCTTCAGGTT CACCGAATCA GACCCCTTAG TCTTCTAGT TCTTCTAGT TCTTCTAGT TCTTCTAGT
 2301 GTGAGGAAGA AGGCGGGGA GAACCTTCTT TCAGGAGGAA CCTTGAACCTT CAGCTTGA TACTGACAT TCTCCAACTT CCACTGGCT
 CACCTCTCT TCCCGGCTT CTGGAAGAA AGTCTCTCTT CAGCTTGA TACTGACAT TCTCCAACTT CCACTGGCT CCACTGGCT CCACTGGCT CCACTGGCT

FIGURE 3A

AL-2b.L 1 CA-CTACAANTAGTBSATCCCCCGGGCTGGAGSAATTTCGACGJCCCT

AL-2b.L 51 G3AAGBBCTCTGG-SSGGGTGAGCGCTCTGCCCGGGGGGGCGCCCTADAG

AL-2b.L 121 CARGGAAGCAGGTCCGCGCTGGGGCTGGGGGGCATCAGCTACCGSGGTGGTC

AL-2b.L 151 CGGGCTGAAGAGGCCAGGCAGCCCAAGGCAGCCACCCCSGGGGGTSCCCSAC

AL-2b.L 221 TTTGGBBBAG-2G-SCCCCCGGGGCCCAAGGGCTTGGCGGGGTCA-GGGGC

AL-2b.L 251 CCCCCCATTTCTSGGCGGGGGGGGGTGGGAGTCGGGGCCCTGCTGC-GCTG

AL-2b.L 321 GGGGTTTTTGGGGGTGGTGTCTGGGGTCAGCCTGGAGCCTGTCT-CTGGAA

AL-2b.L 351 CTGGGCGAATAAGAGGTTTCCAGGCAGAGGGGTGGTTATCTGC-CTACCCCTC

AL-2b.L 421 AGATCGGGGACDGGGTAGACCTGCTCTGCCCGCGCGCGGGGCTCCTGGC

AL-2b.L 451 CCTCACTCCTCTCTC-AATTATGAGTCTTACAAGCTGTAGCTGGTAGGGGG

AL-2b.L 521 TGGTCAGG GCGCG GCGTGTGAGGCGAGCCCTGGCCCAAACTCTCTCTCA
H10036 1 - - - - - GCGCGA GCGTGTGAGGCGAGCCCTGGCCCAAACTCTCTCTCA

AL-2b.L 551 CTGTGTGATCGGGCAGACCTGGATCTCCGCTTCCCATCAAACT-CCAGGAG
H10036 43 CTGTGTGATCGGGCAGACCTGGATCTCCGCTTCCCATCAAGTTCCAGGAG

AL-2b.L 621 TATAGCCCTAACTGTGGGGCCACGAGTTCGGCTCGCACCAAGATTACTA
H10036 93 TATAGCCCTAACTGTGGGGCCACGAGTTCGGCTCGCACCAAGATTACTA

AL-2b.L 651 CATCATTCGCACATCGGATGGGACCCGGGGAGG GCTGGAGAGCC-SCAGG
H10036 141 CATCATTCGCACATCGGATGGGACCCGGGGAGG GCTGGAGAGCC-SCAGG

AL-2b.L 721 GAGGTGTGTGCGCTAACGAGAGGCATGAAGGTGCTTCTCCGAGTGGGACAA
H10036 252 GAGGTGTGTGCGCTAACGAGAGGCATGAAGGTGCTTCTCCGAGTGGGACAA

AL-2b.L 751 AGTC CCGGAGGAGGGGGCTGTCCCGGSAAGACCTG-CTGTGAAATGCCAT
H10036 241 AGTC CCGGAGGAGGGGGCTGTCCCGGSAAGACCTG-CTGTGAAATGCCAT

AL-2b.L 821 GGAAGAGAGACCGAGGGGGCAGCCACAGCCCT-GBAGCCT-GGGAAGCAGAA
H10036 252 GCAAGAGAGACCGAGGGGGCAGCCACAGCCCT-GBAGCCT-3GGGAAGCAGAA

AL-2b.L 841 CTTGCCAGGTGACCCCAACAGCAATGCAACCTCCGGGGT-CCCTGAAGG
H10036 342 CTTGCCAGGTGACCCCAACAGCAATGCAACCTCCGGGGTTCCTTGAAGG

AL-2b.L 907 CCCCC- - GCGGCC CCGAGCA-TGCC TSCAGT- - GGGTGGGGCAGCA G
H10036 352 CCCCC- - GAGCCCTT CCGAGCAIT TCC TSCAN TGG TTT GGGGCAAGCA NG

AL-2b.L 947 GGGGCT- - TGGG GGTGCTCTTGGTGGGGCTGGGAGGGCC-GGGGGTCC
H10036 442 GGGGCT- - TGGG

AL-2b.L 998 A-CTGTGGGGGAGAGGGGGGGGCAAGCCTTCGGAGAGTCCGCAACCTGG

AL-2b.L 1038 CCTGGCTCC-TGGGAGGGGAGGGGTCTCTGGGCCCTGGGGGCTGGAGGTG

AL-2b.L 1188 GATCGGACCTCCGCTGGAGCCTCGGCAAGGTAGGGATAGG-CTGGGC

AL-2b.L 1238 GGTGGGGGGGTGGAGCA-CCCCCTTCTGCCCGCACTATGAGAGGTGAG

10036

lerk2	1	NA	RFGQRWLGKWLVAWVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGG
huHTKL	1	NAY	RRODSYWKYCMGYLMV--LCRTAISKSVLEPIYWNSSVSKFLPGQGG
AL2.shc	1	NG	PPHSGPGGYRYGALLLLGLVLSGL--SLEPYWNSANKRFQAEAG
AL2.long	1	NG	PPHSGPGGYRYGALLLLGLVLSGL--SLEPYWNSANKRFQAEAG

lerk2	32	LV	IPKIGDKLDIICPRA--EAGR--PYEYKLYLVRPQAAACSTVLQ
huHTKL	43	LV	LPQIGDKLDIICPKY--DRTYGYEYKYVMVQKQADRCTIKKE
AL2.shc	49	YV	LPQIGDRLDLLCPRARPPGPHSGPKYEFYKLYLVGGAGGRRCEAPPA
AL2.long	49	YV	LPQIGDRLDLLCPRARPPGPHSGPNVEFYKLYLVGGAGGRRCEAPPA

lerk2	95	PNV	LVTCHAPGEIRFTIKFOEFSPNYMGLFKKHNDYYITSTNGSLEG
huHTKL	96	NT	PLLNCAPDODIKFTIKFOEFSPNLWGLEFQKHNDYYIISTNGSLEG
AL2.shc	96	PN	LLLTCDRPLDLRFTIKFOEYSPNLWGHEFRSHNDYYIATSDGTREG
AL2.long	96	PN	LLLTCDRPLDLRFTIKFOEYSPNLWGHEFRSHNDYYIATSDGTREG

lerk2	145	LEN	REGGVCRTRTKI:MKVCOCNNAVTPSOLTTSRPSKEADNTYKMATO
huHTKL	145	LD	NQSGGVCTRAMKILMKVGDAAG--AOSTRWKCPTRRFELEAG
AL2.shc	145	LE	SLGGGVCLTRGMKVLLRVGGSPRGGAYPKPVSEMPNERDAGAAHSLE
AL2.long	145	LE	SLGGGVCLTRGMKVLLRVGGSPRGGAYPKPVSEMPNERDAGAAHSLE

lerk2	195	AP	GRSLQDSGKHETVNCIEKSGPGASGGGSQDPOGFHNSKVALCAAY
huHTKL	199	TH	GRASSTTSFPYKPMFGSSTGONBAQNSQ--NNILGSEVALPAGI
AL2.shc	199	PG	KENLPQDPTSA-SRQAEGLPPFSPNPAYAGAAGGL--ALLLLGVA
AL2.long	199	PG	KENLPQDPTSA-SRQAEGLPPFSPNPAYAGAAGGL--ALLLLGVA

lerk2	243	GAG	GVIFLLIIFLTVLLKLRLKRRKHTQ-ORAAALSLSLTLASPKGG38
huHTKL	232	AS	GCIFIVIIITLVVLLKTYRRRRKHS-CHTTLSLSLTLATPKRSGN
AL2.shc	244	GAG	GA----MCWRRRRRAKPSERHPPGGSFGRGGSGLGLGG----GGGM3
AL2.long	244	GAG	GA----MCWRRRRRAKPSERHPPGGSFGRGGSGLGLGG----GGGM3

lerk2	294	TA	GTSPSDIIPLR--TTENNYCPHYEKVSGCYGHPVYIVOEMPPOS PA
huHTKL	292	NN	GSFSPSDIIPLR--TADSFCPHYEKVSGCYGHPVYIVOEMPPOS PA
AL2.shc	295	PRE	AEPGELGIALRGGAADFFFCPHYEKVSGCYGHPVYIVODGPPOSP
AL2.long	295	PRE	AEPGELGIALRGGAADFFFCPHYEKVSGCYGHPVYIVODGPPOSP

lerk2	341	N	YYY-----
huHTKL	338	N	YYY-----
AL2.shc	339	N	YYY-----
AL2.long	339	N	YYYTSISVLEWPIILHTIQLFFWRSKCSRVTTFLFPVOVITSTCRMTSF

lerk2	345		KV-----
huHTKL	332		KV-----
AL2.shc	335		KV-----
AL2.long	345	S	FTTLNPSMOACRAQMGFAIRHCFWGDRILOTALPYLVLLILLBRENMH

AL2.long	435	O	TTLRORASYEAEAGONGPL
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FIGURE 4

LERK2.1 1 MA- R P G Q R W L G K W L V A M V V W A L C R L A T P L A K N L E P V S W S S L N P K F L S G K G
huHTKL 1 M A V R R D S V W K Y C W G V L M Y - - L C R T A I S K S I V L E P I Y W N S S N S K F L P G G G
ALII.long 1 M G P P H S G P - G G Y R V G A L L L - - L G V L G L V S G L S L E P V Y W N S A N K R F Q A E G G

LERK2.1 50 L V I Y P K I G D K L D I I C P R A - - - E A G R - - P Y E Y K L Y L V R P E Q A A A C S T V L D
huHTKL 48 L V L Y P Q I G D K L D I I C P K V - - - D S K T V G O Y E Y K Y Y M V D K D Q A D R C T I K K E
ALII.long 48 Y V L Y P Q I G D R L D L L C P R A R P P G P H S S P N Y E F Y K L Y L V G G A Q G R R C E A P P A

LERK2.1 95 P N V L V T C N R P E Q E I R F T I K F Q E F S P N Y M G L E F K K H H D Y Y I T S T S N G S L E G
huHTKL 95 N T P L L N C A K P D Q D I K F T I K F Q E F S P N L W G L E F Q K N K D Y Y I I S T S N G S L E G
ALII.long 98 P N L L L T C D R P D L D L R F T I K F Q E Y S P N L W G H E F R S H H D Y Y I I A T S D G T R E G

LERK2.1 145 L E N R E G G V C R T R T M K I I M K V G O D P N A V T P E O L T T S R P S K E A D N T V K M A T O
huHTKL 145 L D N Q E G G V C O T R A M K I L M K V G O D A S S - - - - - A G S T R N K D P T R R P E L E A G
ALII.long 148 L E S L O G G V C L T R G M K V L L R V G O S P R - - - - - G G A V P R K P V S E M P M E - R

LERK2.1 195 A P G S R G S L G D S D G K H E T Y N Q E E K S G P G A S G G S S G D P D G F F N S K V A L F A A V
huHTKL 189 T N G - R S S T T S P F V K P N P G S S T D G N S A G H S G - - - - - N N I L G S E V A L F A G I
ALII.long 189 D R G A A H S L E P G K E N L P G D P T S N A T S R G A E G - - - - - P L P P P S M P A V A G A

LERK2.1 245 G A G C V I F L L I I I F L T V L L L K L R K R H R K H T O R A A A L S L - - - S T L A S P K G G
huHTKL 232 A S G C I I F I V I I I T L V V L L L K Y R R R H R K H S P Q H T T T L S L - - - S T L A T P K R S
ALII.long 232 A G G L A L L L L G V A G A G G A M C W R R R R A K P S E S R M P G P G S F G R G G S L G L G G G G

LERK2.1 292 S - G T A G T E P S D I I I P L R - - - T E N N Y C P H Y E K V S G D Y G H P V Y I V O E M P P O
huHTKL 279 G - N N N G S E P S D I I I P L R - - - T A D S V F C P H Y E K V S G D Y G H P V Y I V O E M P P O
ALII.long 282 G M G P R E A E P G E L G I A L R G G G A A D P P F C P H Y E K V S G D Y G H P V Y I V O D G P P O

LERK2.1 338 S P A N I Y Y - - - - -
huHTKL 325 S P A N I Y Y - - - - -
ALII.long 332 S P P N I Y Y T S I S V L E W P I L H T I O L F F M R S K C S R V T T F L P P V O V I T T S T C R M

LERK2.1 345 - - - - - K V - - - - -
huHTKL 332 - - - - - K V - - - - -
ALII.long 382 T S F S F T T L N P S M Q A C R A O M G E F R I R W C F W G D R I L G T A L F V L V L I L L L G R L

ALII.long 432 N M H O T T L L R O R A S V E A E A G O H G P L

FIGURE 5